



FIG. 1A
FIG. 1B
FIG. 1C

Top: protein produced from cDNA clone A1
Mid: protein produced from Roche patent bovine liver sequence
Bot: protein produced from Roche patent human liver sequence

FIG. 1

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SEQ ID NO: 4 MSAFRLWPGLLIMLG-SLCHRGSPCGLSTHIEIGHRALEFFLQHNGRVNYRELLLEHQDA
SEQ ID NO: 5 MSAFRFWSGLMLLG-FLCPRSSPCGISTHIEIGHRALEFFLHLQDGSINYKELLRLRHQDA
SEQ ID NO: 6 MSAFRLWPGLLMIVMASLCHRGSSCGLSTHIEIGHRALEFFLHLHNGHVNYKELLLEHQDA

YQAGIVFPDCFYPSICKGKFHDVSESTHWTPFLNASVHYIRENYPLPWEKDEKLVAF
YQAGSVFPDSFYPSICERGQFHDVSESTHWTPFLNASVHYIRKNYPLPWDEDTEKLVAF
YQAGTVFPDCFYPSLCKGKFHDVSESTHWTPFLNASVHYIRENYPLPWEKDEKLVAF

FGITSHMAADVSWHSLGLEQQLRTMGAIDFHGCSYSEAHSAAGDFGGDVLSEFFNFNYLA
FGITSHMADVNVHSLGIENGFLRTMAAIDFHNSYPEAHPAGDFGGDVLSEFFKFNLYS
FGITSHMADVSWHSLGIEQQLRTMGAIDFHGCSYSEAHSAAGDFGGDVLSEFFNFNYLA

FIG. 1A

RRWYVPVKDLLGIYEKLYGRKVIITENVIVDCSHIQFLEMYGEMLAVSKLYPTYSTKSPFL
RHWYVPAEDLLGIYRELYGRIVITTKKAIVDCSYLQFLEMYAEMLAISKLYPTYSVKSPFL
RRWYVPVKDLLGIYEKLYGREVITENVIVDCSHIQFLEMYGEMLAVSKLYPSYSTKSPFL

VEQFQEYFLGGLDDMAFWSTNIYHLTSFMLENGTSDCNLPENPENPLFIACGGQQNNHTQG
VEQFQEYFLGGLDDMAFWSTNIYHLTSMLKNGTSNCNLPENP--LFTTCGGQQNNHTG
VEQFQEYFLGGLDDMAFWSTNIYHLTSFMLENGTSDCSLFENPENPLFIACGGQQNNHTQG

SKMQKNDFHRNLTTSLTESVDRNINNYTERGVFFSVNSWTPDMSFIYKALERNVRTMFIG
SKVQKNGFHKNVTAALTKNIGKHINYYTKRGVFFSVDSWTPDMSFIYKALERNVRTMFIG
SKMQKNDFHRNLTTSSLTENIDRNINNYTERGVFFSVNSWTPDMSFIYKALERNVRTMFIG

GSQLSQKHVSPLASYFLSFPPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGRIHIGRV
SSQP-LTHVSSPAASYLSFPYTRLGWAMTSADLNQDGYGDLVVGAPGYSHPGRIHVGRV
GSQLSQKHISSPLASYFLSFPPYARLGWAMTSADLNQDGYGDLVVGAPGYSRPGRIHIGRV

YLIYGNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDFNVDPDLAVGAPSVGS
YLIYGNDLG-PRIDLDDKEAHGILEGFQPSGRFGSAVAVLDFNVDPDLAVGAPSVGS
YLIYGNELGLPPVDLDDKEAHGILEGFQPSGRFGSALAMLD FNMMDGVDPDLAVGAPSVGS

EQLTYKGAVYVYFGSKQGMSSSPNITISCQDIYCNLGTLLAADVNGDSEPD-LVIGSP
EKLTYTGAVYVYFGSKQQLSSSPNVTISCQDIYCNLGTLLAADVNGDSEPD-LVIGSP
EQLTYKGAVYVYFGSKQGRMSSSPNITISCQDIYCNLGTLLAADVNGDSEPD-LVIGSP

FIG. 1B

FAPGGKQKGI VAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTLL
 FAFGGKQKGI VAAFYSGSSYSREKLNVEAANWVMVKEEDFAWLGYSLHGVNVNRTLL
 FAPGGKQKGI VAAFYSGPSLSNKEKLNVEAANWTVRGEEDFAWFGYSLHGVTVDNRTLL

LVGSPTWKNASRLGHLHIRDEKKS LGRVGYFPPNGQSWFTISGDKAMKLGTSLS SGH
 LAGSPTWKDTSSQGH LFRTRDEKQSPGRVGYFPPI CQSWFTISGDKAMKLGTSLS SGH
 LVGSPTWKNASRLGRLHIRDEKKS LGRVGYFPPNSQSWFTIVGDKAMKLGTSLS SGH

VLMNGTLKQVLLVGAPTYDDVSKVAFLTVTLHQGGATRMVALISDAQPLLLSTFSGDRRF
 VIVNGTRTQVLLVGAPTQDVVSKS - FLTMTLHQGGSTRMYELTPDSQPSLLSTFSGNRRF
 VLMNGTLTQVLLVGAPTRDDVSKMAFLTMTLHQGGATRMVALTSDLQPPLLSTFSGDRRF

SRFGGVLHLSDDLDDGLDEI IMAAPLRIADVTSLIGGEDGRVYVYNGKETTLGDMTGKC
 SRFGGVLHLSDDLNDGLDEI IVAAPLRIADTAGLMGEEDGRVYVFNGKQITVGDVTGKC
 SRFGGVLHLSDDLDDGVDEI IVAAPLRIADVTSLIGGEDGRVYVYNGKETTLGDMTGKC

KSWITPCPEEKAQYVLISPEASSRFGSSLI TVRSKAKNQVIAAGRSSLGARLSGALHVY
 KSWVTPCPEEKAQYVLISPEAGSRFGSSVITVRSKEKNQVIAAGRSSLGARLSGVLHIY
 KSWMTPCPEEKAQYVLISPEASSRFGSSLI TVRSKAKNQVIAAGRSSLGARLSGALHVY

SLGSD
 RLQD
 SLGSD

FIG. 1C

FIG. 2A
FIG. 2B
FIG. 2C
FIG. 2D
FIG. 2E
FIG. 2F
FIG. 2G
FIG. 2H
FIG. 2I
FIG. 2J
FIG. 2K

FIG. 2

Top: pancreatic-form cDNA sequence from GenBank database SEQ ID NO: 7
mid: our sequence cloned from human liver cDNA library SEQ ID NO: 8
bot: Roche patent pancreatic-form partial cDNA sequence SEQ ID NO: 9

1	GTGACCTGCTTAGAGAGAAAGCGGTGGTCTGCACCTGGATTTTGGAGTCCCAGTGCTGCT	60

1	-----ATGTCTGCT	9
61	GCAGCTCTGAGCATTTCCACGTCAACAGAGAAGCCGGTGGCAATGAGAGCATGTCTGCT	120

FIG. 2A

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10  TTCAGGTTGTGGCCTGGCCTGCTGATCATGTTGGGTTCTCTCTGCCATAGAGGTTCAACG 69
121 TTCAGGTTGTGGCCTGGCCTGCTGATCATGTTGGGTTCTCTCTGCCATAGAGGTTCAACG 180
-----

70  TGTGGCCTTTCAACACACACGTAGAAATAGGACACAGAGCTCTGGAGTTTCTTCAGCTTCAC 129
181 TGTGGCCTTTCAACACACACATAGAAATAGGACACAGAGCTCTGGAGTTTCTTCAGCTTCAC 240
-----

130 AATGGGCGTGTTAACTACAGAGAGCTGTACTAGAACACCCAGGATGCGTATCAGGCTGGA 189
241 AATGGGCGTGTTAACTACAGAGAGCTGTACTAGAACACCCAGGATGCGTATCAGGCTGGA 300
-----

190 ATCGTGTTTCCTGATTGTTTTTACCCTAGCATCTGCAAGGAGGAAATTCATGATGTG 249
301 ATCGTGTTTCCTGATTGTTTTTACCCTAGCATCTGCAAGGAGGAAATTCATGATGTG 360
-----

250 TCTGAGAGCACTCACTGGACTCCGTTTCTTAATGCAAGCGTTCATTATATCCGAGAGAAC 309
361 TCTGAGAGCACTCACTGGACTCCGTTTCTTAATGCAAGCGTTCATTATATCCGAGAGAAC 420
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FIG. 2B

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310 TATCCCCCTTCCCTGGGAGAGGACACAGAGAAACTGGTAGCTTTCCTTGTGGAATTACT 369
421 TATCCCCCTTCCCTGGGAGAGGACACAGAGAAACTGGTAGCTTTCCTTGTGGAATTACT 480
-----
370 TCTCACATGGCGGCAGATGTCAGCTGGCATACTCTGGGCCCTTGAAACAAGGATTCCTTAGG 429
481 TCTCACATGGCGGCAGATGTCAGCTGGCATACTCTGGGCCCTTGAAACAAGGATTCCTTAGG 540
-----
430 ACCATGGGAGCTATTGATTTTCACGGCTCCTATTTCAGAGGCTCATTCGGCTGGTGATTTT 489
541 ACCATGGGAGCTATTGATTTTCACGGCTCCTATTTCAGAGGCTCATTCGGCTGGTGATTTT 600
-----
490 GGAGGAGATGTGTGAGCCAGTTTGAAATTTTAATTTAATTACCTTGACACGACGCTGGTAT 549
601 GGAGGAGATGTGTGAGCCAGTTTGAAATTTTAATTTAATTACCTTGACACGACGCTGGTAT 660
-----
550 GTGCCAGTCAAAGATCTACTGGGAATTTATGAGAAACTGTATGGTCGAAAAGTCATCACC 609
661 GTGCCAGTCAAAGATCTACTGGGAATTTATGAGAAACTGTATGGTCGAAAAGTCATCACC 720
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FIG. 2C

610	GAAATGTAATCGTTGATTGTTCA	669
721	GAAATGTAATCGTTGATTGTTCA	780

670	GCTGTTTCCAAAGTTATATCCCA	729
781	GCTGTTTCCAAAGTTATATCCCA	840

730	CAAGAGTATTTTCTTGGAGGACT	789
841	CAAGAGTATTTTCTTGGAGGACT	900

790	CTAACAAATCTTCATGTTGGAGA	849
901	CTAACAAAGCTTTCATGTTGGAG	960

850	TTCAATTGCATGTGGCGGCCAGCA	909
961	TTCAATTGCATGTGGCGGCCAGCA	1020

910	TTTCACAGAAATTTGACTACATCC	969
1021	TTTCACAGAAATTTGACTACATCC	1080

970 GAAAGAGGAGTGTCTTTAGTGTAAATTCCTGGACCCCGGATTCCATGTCCTTTATCTAC 1029
1081 GAAAGAGGAGTGTCTTTAGTGTAAATTCCTGGACCCCGGATTCCATGTCCTTTATCTAC 1140

1030 AAGGCTTTGGAAAGGAACATAAGGACAATGTTCATAGGTGGCTCTCAGTTGTCACAAAG 1089
1141 AAGGCTTTGGAAAGGAACATAAGGACAATGTTCATAGGTGGCTCTCAGTTGTCACAAAG 1200

1090 CACGTCTCCAGCCCCCTTAGCATCTTACTTCTTGTCAATTTCCTTATGCGAGGCTTGGCTGG 1149
1201 CACGTCTCCAGCCCCCTTAGCATCTTACTTCTTGTCAATTTCCTTATGCGAGGCTTGGCTGG 1260

1150 GCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGTGGGCGCACCA 1209
1261 GCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGTGGGCGCACCA 1320

1210 GGCTACAGCCGCCCGCCACATCCACATCGGGCGGTGTACCTCATCTACGGCAATGAC 1269
1321 GGCTACAGCCGCCCGCCACATCCACATCGGGCGGTGTACCTCATCTACGGCAATGAC 1380

1270 CTGGGCCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCACAGGATCCTTGAAGGC 1329
1381 CTGGGCCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCACAGGATCCTTGAAGGC 1440

FIG. 2E

1330 TTCAGCCCTCAGGTCGGTTTGGCTCGGCCTTGGCTGTGTGGACTTTAAACGTGGACGGC 1389
1441 TTCAGCCCTCAGGTCGGTTTGGCTCGGCCTTGGCTGTGTGGACTTTAAACGTGGACGGC 1500

1390 GTGCCTGACCTGGCCGTGGAGCTCCCTCGGTGGGCTCCGAGCAGCTCACCTACAAAGGT 1449
1501 GTGCCTGACCTGGCCGTGGAGCTCCCTCGGTGGGCTCCGAGCAGCTCACCTACAAAGGT 1560

1450 GCCGTGTATGTCTACTTTGGTTCCAAACAAGGAGGAATGTCTTCTTCCCCTAACATCACC 1509
1561 GCCGTGTATGTCTACTTTGGTTCCAAACAAGGAGGAATGTCTTCTTCCCCTAACATCACC 1620

1510 ATTTCTTGCCAGGACATCTACTGTAACTTGGGCTGGACTCTCTTGGCTGCAGATGTGAAT 1569
1621 ATTTCTTGCCAGGACATCTACTGTAACTTGGGCTGGACTCTCTTGGCTGCAGATGTGAAT 1680

1570 GGAGACAGTGAACCCGATCTGTGTCATCGGCTCCCCTTTTGACCCAGGTGGAGGGAAGCAG 1629
1681 GGAGACAGTGAACCCGATCTGTGTCATCGGCTCCCCTTTTGACCCAGGTGGAGGGAAGCAG 1740

1630 AAGGGAATTGTGGCTGCGTTTATTCTGGCCCCAGCCTGAGCGACAAAGAAAACCTGAAC 1689
1741 AAGGGAATTGTGGCTGCGTTTATTCTGGCCCCAGCCTGAGCGACAAAGAAAACCTGAAC 1800
1 -----CTGGCCCCAGCCTGAGCGACAAAGAAAACCTGAAC 35

FIG. 2F

1690 GTGGAGGCAGCCAACTGGACGGTGAGAGGCGAGGAAGACTTCTCCTGGTTTGGATATTCC 1749
1801 GTGGAGGCAGCCAACTGGACGGTGAGAGGCGAGGAAGACTTCTCCTGGTTTGGATATTCC 1860
36 GTGGAGGCAGCCAACTGGACGGTGAGAGGCGAGGAAGACTTCTCCTGGTTTGGATATTCC 95

1750 CTTACCGGTGTCACTGTGGACAACAGAAACCTTGCTGTTGGTGGAGCCCGACCTGGAAG 1809
1861 CTTACCGGTGTCACTGTGGACAACAGAAACCTTGCTGTTGGTGGAGCCCGACCTGGAAG 1920
96 CTTACCGGTGTCACTGTGGACAACAGAAACCTTGCTGTTGGTGGAGCCCGACCTGGAAG 155

1810 AATGCCAGCAGGCTGGGCCATTGTGTTACACATCCGAGATGAGAAAAGAGCCTTGGGAGG 1869
1921 AATGCCAGCAGGCTGGGCCATTGTGTTACACATCCGAGATGAGAAAAGAGCCTTGGGAGG 1980
156 AATGCCAGCAGGCTGGGCCATTGTGTTACACATCCGAGATGAGAAAAGAGCCTTGGGAGG 215

1870 GTGTATGGCTACTTCCCACCAAACGGCCAAAGCTGGTTTACCATTCTGGAGACAAGGCA 1929
1981 GTGTATGGCTACTTCCCACCAAACGGCCAAAGCTGGTTTACCATTCTGGAGACAAGGCA 2040
216 GTGTATGGCTACTTCC - ACCAAACGGCCAAAGCTGGTTTACCATTCTGGAGACAAGGCA 275

1930 ATGGGGAAACTGGGTACTTCCCTTTCCAGTGGCCACGTA CTGATGAATGGGACTCTGAAA 1989
2041 ATGGGGAAACTGGGTACTTCCCTTTCCAGTGGCCACGTA CTGATGAATGGGACTCTGAAA 2100
276 ATGGGGAAACTGGGTACTTCCCTTTCCAGTGGTCACGTA CTGATGAATGGGACTCTGAAA 335

1990 CAAGTGCTGCTGTTGGAGCCCCCTACGTACGATGACGTGCTAAGGTGGCATTCCTGACC 2049
2101 CAAGTGCTGCTGTTGGAGCCCCCTACGTACGATGACGTGCTAAGGTGGCATTCCTGACC 2160
336 CAAGTGCTGCTGTTGGAGCCCCCTACGTACGATGACGTGCTAAGGTGGCATTCCTGACC 395

FIG. 2G

2050 GTGACCCCTACACCAAGGCGGAGCCACTCGCATGTACGCACTCATATATCTGACGCGCAGCCT 2109
2161 GTGACCCCTACACCAAGGCGGAGCCACTCGCATGTACGCACTCATATATCTGACGCGCAGCCT 2220
396 GTGACCCCTACACCAAGGCGGAGCCACTCGCGTGTACGCACTCATATATCTGACGCGCAGCCT 455

2110 CTGCTGCTCAGCACCTTCAGCGGAGACCGCGCTTCTCCGATTTGGTGGCGTTCTGCAC 2169
2221 CTGCTGCTCAGCACCTTCAGCGGAGACCGCGCTTCTCCGATTTGGTGGCGTTCTGCAC 2280
456 CTGCTGCTCAGCACCTTCAGCGGAGACCGCGCTTCTCCGATTTGGTGGCGTTCTGCAC 515

2170 TTGAGTGACCTGGATGATGGCTTAGATGAAATCATCATGGCAGCCCCCTGAGGATA 2229
2281 TTGAGTGACCTGGATGATGGCTTAGATGAAATCATCATGGCAGCCCCCTGAGGATA 2340
516 TTGAGTGACCTGGATGATGGCTTAGATGAAATCATCATGGCAGCCCCCTGAGGATA 575

2230 GCAGATGTAACCTCTGGACTGATTGGGGGAGAAAGACGGCCGAGTATATGTATATAATGGC 2289
2341 GCAGATGTAACCTCTGGACTGATTGGGGGAGAAAGACGGCCGAGTATATGTATATAATGGC 2400
576 GCAGATGTAACCTCTGGACTGATTGGGGGAGAAAGACGGCCGAGTATATGTATATAATGGC 635

2290 AAAGAGACCAACCCTTGGTGACATGACTGGCAAATGCAAATCATGGATAAATCCATGTCCA 2349
2401 AAAGAGACCAACCCTTGGTGACATGACTGGCAAATGCAAATCATGGATAAATCCATGTCCA 2460
636 AAAGAGACCAACCCTTGGTGACATGACTGGCAAATGCAAATCATGGATAAATCCATGTCCA 695

2350 GAAGAAAAGGCCCAATATGTATTGATTTCTCCTGAAGCCAGCTCAAGGTTTGGGAGCTCC 2409
2461 GAAGAAAAGGCCCAATATGTATTGATTTCTCCTGAAGCCAGCTCAAGGTTTGGGAGCTCC 2520
696 GAAGAAAAGGCCCAATATGTATTGATTTCTCCTGAAGCCAGCTCAAGGTTTGGGAGCTCC 755

FIG. 2H

2410 CTCATCACCGTGAGGTCCAAGGCAAGAACCAAGTCGTCAATTGCTGCTGGAAGGAGTTCT 2469
2521 CTCATCACCGTGAGGTCCAAGGCAAGAACCAAGTCGTCAATTGCTGCTGGAAGGAGTTCT 2580
756 CTCATCACCGTGAGGTCCAAGGCAAGAACCAAGTCGTCAATTGCTGCTGGAAGGAGTTCT 815

2470 TTGGGAGCCCGACTCTCCGGGGCAGCTTACGCTCTATAGCCTTGGCTCAGATTGAAGATTT 2529
2581 TTGGGAGCCCGACTCTCCGGGGCAGCTTACGCTCTATAGCCTTGGCTCAGATTGAAGATTT 2640
816 TTGGGAGCCCGACTCTCCGGGGCAGCTTACGCTCTATAGCCTTGGCTCAGATTGAAGATTT 875

2530 CACTGCATTTCCCCACTCTGCCCCACCTCTCTCATGTGCTGAATCACATCCATGGTGAGCATT 2589
2641 CACTGCATTTCCCCACTCTGCCCCACCTCTCTCATGTGCTGAATCACATCCATGGTGAGCATT 2700
876 CACTGCATTTCCCCACTCTGCCCCACCTCTCTCATGTGCTGAATCACATCCATGGTGAGCATT 935

2590 TTGATGGACAAAGTGGCACATCCAGTGGAGCGGTGTAGATCCTGTATAGACATGGGGCTC 2649
2701 TTGATGGACAAAGTGGCACATCCAGTGGAGCGGTGTAGATCCTGTATAGACATGGGGCTC 2760
936 TTGATGGACAAAGTGGCACATCCAGTGGAGCGGTGTAGATCCTGTATAGACATGGGGCTC 995

2650 CTGGGA----- 2655
2761 CTGGGA----- 2766
996 CTGGGACAGTGAAACCGATCTGGTCATCGGCTCCCCCTTTTGACCAAGGTGGAGGGAAGCA 1055

2656 -----GTAGAGAGACACACTAACAGCCACACCCCTCTG 2687
2767 -----GTAGAGAGACACACTAACAGCCACACCCCTCTG 2798
1056 GAAGGGAATTGTGGCTGCGTTTATTGAGTAGAGAGACACACTAACAGCCACACCCCTCTG 1115

FIG. 21

2688 GAAATCTGATACAGTAAATATATGACTGCACCAGAAATATGTGAAATAGCAGACATTCTG 2747
2799 GAAATCTGATACAGTAAATATATGACTGCACCAG----- 2833
1116 GAAATCTGATACAGTAAATATATGACTACACCAGAAATATGTGAAATAGCAGACATTCTG 1175

2748 CTTACTCATGTCCTTCCACAGTTTACTTCCTCGCTCCCTTTGCATCTAAACCTTTCTT 2807

1176 CTTACTCATGTCCTTCCACAGTTTACTTCCTCGCTCCCTTTGCATCTAAACCTTTCTT 1235

2808 CTTTCCCACTTATTGCCGTGTAGTCAGACCTGCTGTACAACCTATTTCCTCTTCCCTCTTG 2867

1236 CTTTCCCACTTATTGCCGTGTAGTC----- 1261

2868 AATGTCTTTCCAGTGGCTGGAAAGTCCCTCTGTGTTATCTGTTAGAACAGTCTCTGTA 2927

2928 CACAAATTCCTCTAAACATCCTTTTTTAAATAAGAAATTGTTTCAGCCATAAAGAAAGA 2987

2988 ACAAGATCATGCCCTTTGCAGGGACATGGATGGAGCTGGAGGCCATTATCCTTCATAAAC 3047

FIG. 2J

3048 TATTGCAGGAACAGAAAAACCAACTCCATATTCTCACTTGTAAGTGGGAGCTAAGTGA 3107

3108 GAACACGTGGACACATAGAGGGAAACAACACACACTGGGGCCCTATGAGAGGGCGGAAGGT 3167

3168 GGGAGGAGGAGAGATCAGGAAAAATAACTAATGGATACTTAGGGTGATGAAAATAATCTG 3227

3228 TGTAACAAACCCCATGACACACCTTTATGTATGTAACAACACGCACTTCCTGCGCATG 3287

3288 TACCCCTGAACTTAAAAGTTAAAAAAGTTGAACTTAAAAATAACAGATTGGCCCATGC 3347

3348 CAATCAAAGTATAATAGAAAGCATAGTATAC 3378

FIG. 2K

FIG. 3A
FIG. 3B
FIG. 3C

FIG. 3

SEQ ID NO: 10

cDNA clone d3

MILLFQDSMSFYKALERNIRTMFIGGSQLSQKHVSSPLASYFLSFPYARLGWAMTSADL
 NQDGHGDLVVGAPGYSRPGHIHIGRVYLIYGNDLGLPPVDLDDKEAHRILEGFQPSGRF
 GSALAVLDFNVDPDLAVGAPSVGSEQLTKGAVYVYFGSKQGMSSSPNITISCQDIYC
 NLGWTLLAADVNGDSEPDLVIGSPFAPGGGKQKGI VAAFYSGPSSLSDKEKLNVEAANWTV
 RGEEDFSWFGYSLHGVTVDNRTLLLVGSPTWKNASRLGHLLHIRDEKKS LGRVYGYFPPN
 GQSWFTISGDKAMGKLGTSLSGGHVLNMGTLKQVLLVGAPTYDDVSKVAFLT VTLHQGGA
 TRMYALISDAQPLLLSTFSGDRRFRFGGVLHLSDDLDDGLDEI IMAAPLRIADVTSGLI
 GGEDGRVYVYNGKETTLGDMTGKCKSWITPCPEEKAQYVLISPEASSRFGSSLI TVRSKA
 KNQVVIAAGRSSLGARLSGALHVYSLGSD

FIG. 3A

SEQ ID NO: 11

cdna clone b2

MSAFRLWPGLLLIMGLSLCHRGSPCGLSTHIEIGHRALEFLQLHNGRVNRYRELLLEHQDAY
QAGIVFPDCFYPSICKGKFHDVSESTHWTPFLNASVHYIRENYPLPWEKDTTEKLVAFLF
GITSHMAADVSWHSLGLEQGLRTMGAIDFHGYSYSEAHSAAGDFGSDVLSQFEFFNFNYLAR
RWYVPVKDLLGIYEKLYGRKVI TENVI VDCSHIQFLEMYGEMLA VSKLYPTYSTKSPFLV
EQFQEYFLGGLDDMAFWSTNIYHLTSEMLENGTSDCNLPENPLFIACGGQQNHTQGSKMQ
KNDFHRNLTTSLTESVDRNINITYTERGVFFSVNSWTPDSMSFIYKALERNIRTMFIGGSQL
SQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIY
GNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDENVDGVPDLAVGAPSVGSEQLT
YKGAVVYVFGSKQGMSSSPNITISCQDIYCNLGTLLAADVNGDSEPDLVIGSPFAPGG
GKQKGI VAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTL LLLVGSP
TWKNASRLGHLLHIRDEKKS LGRVYGYFPPNGQSWFTISGDKAMGKLGTSLSSGHVLMNG
TLKQVLLVGAPTYDDVSKVAFLT VTLHQGGATRM YALISDAQPLLLSTFSGDRRFRSFRGG
VLHLSDDLDDGLDEI IMAAPLR IADVTSGLIGGEDGRVYVYNGKETTLGDMTGKCKSWIT
PCPEEKVSEKKKKK

FIG. 3B

SEQ ID NO: 12

cDNA clone a1

MSAFRLWPGLLIMLGSLCHRGSPCGLSTHIEIGHRALEFLQLHNGRVNYRELLLEHQDAY
QAGIVFPDCFYPSICKGKFHDVSESTHWTPFLNASVHYIRENYPLPWEKDTTEKLVAFLF
GITSHMAADVSWHSLGLEQGFRLRTMGAIDFHGSYSEAHSAAGDFGGDVLSQLFEFFNFNYLAR
RWYVPVKDLLGIYEKLYGRKVI TENVI VDCSHIQFLEM YGEMLA VSKLYPTYSTKSPFLV
EQFOEYFLGGLDDMAFWSTNIYHLTSFMLENGTSDCNLPENPLFIACGGQQNHTQGSKMQ
KNDFHRNLTTSLTESVDRNIN YTERGVFFSVNSWTPDMSFIYKALERNIRTMFIGGSQL
SQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIY
GNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDFNVDPDLAVGAPSVGSEQLT
YKGAVVYVYFGSKQGMSSSPNITISCDIYCNLGTWTLAADVNGDSEPDLVIGSPFAPGG
GKQKGI VAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTLLLVGSP
TWKNASRLGHLLHIRDEKKSLGRVYGYFFPPNGQSWFTISGDKAMGKLGTSLSSGHVLMNG
TLKQVLLVGAPTYDDVSKVAFLT VTLHQGGATRM YALISDAQPLLLSTFSGDRRFRSREGG
VLHLSDDLDDGLDEI IMAAPLRIADVTSGLIGGEDGRVYVYNGKETTLGDMTGKCKSWIT
PCPEEKAQYVLI SPEASSRFGSSLITVRSKAKNQV VIAAGRSSLGARLSGALHVYSLGSD

FIG. 3C

FIG. 4A
FIG. 4B
FIG. 4C

FIG. 4

SEQ ID NO: 13

19/41

2832 bp: 690 a 688 c 735 g 719 t

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1  gtgacctgct tagagagaag cggtaggtct gcacctggat ttggagtcc cagtctgct
61  gcagctctga gcattccac gtcaccagag aagccggtgg gcaatgagag catgtctgct
121  ttcaggttgt ggcctggcct gctgatcatg ttgggttctc tctgccatag aggttcaccg
181  tgtggccttt caacacacat agaaatagga cacagagctc tggagtcttc tcagcttcac
241  aatgggctg ttaactacag agagctgtta ctagaacacc aggatgcgta tcaggctgga
301  atcgtgttc ctgattgttt ttaccctagc atctgcaaag gaggaaaatt ccatgatgtg

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FIG. 4A

361 tctgagagca ctcactggac tccgtttctt aatgcaagcg ttcattatat ccgagagaac
421 tatccccttc cctgggagaa ggacacagag aaactggtag ctttcttggt tggattact
481 tctcacatgg cggcagatgt cagctggcat agtctgggcc ttgaacaagg attccttagg
541 accatgggag ctattgattt tcacggctcc tattcagagg ctcatcggc tggatgttt
601 ggaggagatg tgttgagcca gtttgaattt aattttaatt accttgcag acgctggtat
661 gtgccagtca aagatctact gggaatttat gagaaactgt atggtcgaaa agtcatcacc
721 gaaaatgtaa tcgttgattg ttcacatata cagttcttag aaatgtatgg tgagatgcta
781 gctgtttcca agttatatcc cacttactct acaaagtccc cgtttttggg ggaacaattc
841 caagagtatt ttcttggagg actggatgat atggcatttt ggtccactaa tatttaccat
901 ctaacaagct tcatgttga gaatgggacc agtgactgca acctgcctga gaacctctg
961 ttcatgtcat gtggcgcca gcaaaaccac acccagggt caaaaatgca gaaaaatgat
1021 tttcacagaa atttgactac atccctaact gaaagtgttg acaggaatat aaactatact
1081 gaaagaggag tgttctttag tgtaaatcc tggacccccg atttccatgtc ctttatctac
1141 aaggctttgg aaaggaacat aaggacaatg ttcataagtg gctctcagtt gtcacaaaag
1201 cacgtctcca gcccttagc atctacttc ttgtcatttc cttatgcgag gcttggctgg
1261 gcaatgacct cagctgacct caaccaggat gggcacggtg acctcgtggg gggcgaccca
1321 ggctacagcc gccccggcca catccacatc gggcgctgtg acctcatcta cggcaatgac
1381 ctgggacctg cacctgttga cctggacctg gacaaggagg ccacaggat ccttgaaggc
1441 ttccagccct caggtcgggt tggctcgcc ttggctgtgt tggactttaa cgtggacggc
1501 gtgcctgacc tggccgtggg agtccctcg gtgggctccg agcagctcac ctacaaagg
1561 gccgtgtatg tctactttgg ttccaaaaca ggaggaatgt cttcttcccc taacatcacc

FIG. 4B

1621 atttcttgcc aggacatcta ctgtaacttg ggctggactc tcttggctgc agatgtgaat
1681 ggagacagtg aaccgatctt ggtcatcggc tccccttttg caccaggtgg agggaaagcag
1741 aaggaattg tggctgcgtt ttattctggc ccagcctga gcgacaaaga aaaactgaac
1801 gtggaggcag ccaactggac ggtgagaggc gaggaagact tctcctggtt tggatatcc
1861 ctccacggtg tcaactgtgga caacagaacc ttgctgttgg ttgggagccc gacctggaag
1921 aatgccagca ggctgggcca ttgtttacac atccgagatg agaaaaagag ccttgggagg
1981 gtgtatggct acttcccacc aaacggccaa agctgggtta ccatttctgg agacaaggca
2041 atggggaac tgggtacttc cctttccagt ggcacgtac tgatgaatgg gactctgaaa
2101 caagtgtgc tggttggagc ccctacgtac gatgacgtgt ctaagggtggc attcctgacc
2161 gtgaccctac accaaggcgg agccactcgc atgtacgcac tcatatctga cgcgcagcct
2221 ctgctgctca gcaccttcag cggagaccgc cgcttctccc gatttgggtg cgttctgcac
2281 ttgagtgacc tggatgatga tggcttagat gaaatcatca tggcagcccc cctgaggata
2341 gcagatgtaa cctctggact gattggggga gaagacggcc gagtatatgt atataatggc
2401 aaagagacca cccttgggtga catgactggc aaatgcaaat catggataac tccatgtcca
2461 gaagaaaagg cccaatatgt attgatctt cctgaagcca gctcaagggt tgggagctcc
2521 ctcatcaccg tgaggtccaa ggcaaaagaa caagtcgtca ttgctgctgg aaggagtctt
2581 ttgggagccc gactctccgg ggcacttcac gtctatagcc ttggctcaga ttgaagattt
2641 cactgcattt cccactctg cccacctctc tcatgctgaa tcacatccat ggtgagcatt
2701 ttgatggaca aagtggcaca tccagtggag cggtggtaga tcctgataga catggggctc
2761 ctgggagtag agagacacac taacagccac accctctgga aatctgatac agtaaatata
2821 tgactgcacc ag

FIG. 4C

2472 bp: 617 a 588 c 639 g 628 t

FIG. 5A
FIG. 5B

FIG. 5

1 gtctgcacct ggatttttggg gtcccagtgc tgctgcagct ctgagcattc ccacgtcacc
61 agagaagccg gtgggcaatg agagcatgtc tgctttcagg ttgtggcctg gcctgctgat
121 catgttgggt tctctctgcc atagaggttc accgtgtggc ctttcaacac acatagaaat
181 aggacacaga gctctggagt ttcttcagct tcacaatggg cgtgtttaact acagagagct
241 gttactagaa caccaggatg cgtatcaggc tggaatcgtg ttctctgatt gtttttacc
301 tagcatctgc aaaggaggaa aattccatga tgtgtctgag agcactcact ggactccgtt
361 tcttaatgca agcgttcatt atatccgaga gaactatccc ctccctggg agaaggacac
421 agagaaactg gtagctttct tgtttggaaat tacttctcac atggcggcag atgtcagctg
481 gcatagtctg ggccttgaac aaggattcct taggaccatg ggagctattg attttcacgg
541 ctctattca gaggctcatt cggctgggta ttttggagga gatgtgtga gccagtttga
601 atttaatttt aattaccttg cagcagctg gtatgtgcca gtcaaaagatc tactgggaat
661 ttatgagaaa ctgtatggtc gaaaagtcac caccgaaaat gtaatcgttg attgttcaca
721 tatccagttc ttagaaatgt atggtgagat gctagctgtt tccaagtatt atcccactta
781 ctctacaaag tcccgtttt ttgtggaaca attccaagag tattttcttg gaggactgga
841 tgatatggca ttttgggtcca ctaatattha ccactaaca agcttcatgt tggagaatgg
901 gaccagtga c tgcaacctgc ctgagaacct tctgttcatt gcatgtggcg gccagcaaaa
961 ccacacccag ggctcaaaaa tgcagaaaaa tgattttcac agaaatttga ctacatccct
1021 aactgaaagt gttgacagga atataaacta tactgaaaga ggagtgttct ttagtgtaaa
1081 ttcctggacc cggattcca tgcctttat ctacaaggct ttggaaagga acataaggac

FIG. 5A

1141 aatgttcata ggtggctctc agttgtcaca aaagcacgtc tccagccctc tagcatctta
1201 cttcttgtca tttccttatg cgaggcttgg ctgggcaatg acctcagctg acctcaacca
1261 ggatgggcac ggtgacctcg tggtagggcg accaggctac agccgccccg gccacatcca
1321 catcgggcgc gtgtacctca tctacggcaa tgacctgggc ctgccacctg ttgacctgga
1381 cctggacaag gaggcccaca ggatccttga aggttccag ccctcaggtc ggtttggctc
1441 ggccttggct gtgttggact ttaacgtgga cggcgtgcct gacctggccg tgggagctcc
1501 ctcggtgggc tccgagcagc tcacctacaa aggtgccgtg tatgtctact ttggttccaa
1561 acaaggagga atgtcttctt cccctaacat caccatttct tgccaggaca tctactgtaa
1621 cttgggctgg actctcttgg ctgcagatgt gaatggagac agtgaaccg atctggtcat
1681 cggctcccct ttgcaccag gtggaggga gcagaaggga attgtggctg cgttttattc
1741 tggccccagc ctgagcgaca aagaaaaact gaacgtggag gcagccaact ggacggtgag
1801 aggcgaggaa gacttctcct ggtttggata ttcccttcac ggtgtcactg tggacaacag
1861 aaccttgctg ttggttggga gcccagacct gaagaatgcc agcaggctgg gccatttgtt
1921 acacatccga gatgagaaaa agagccttgg gaggtgtat ggctacttcc caccaaacgg
1981 ccaaagctgg ttaccattt ctggagacaa ggcaatgggg aaactgggta ctcccttctc
2041 cagtggccac gtactgatga atgggactct gaaacaagtg ctgctgggtg gagccccctac
2101 gtacgatgac gtgtctaagg tggcattcct gaccgtgacc ctacaccaag gcggagccac
2161 tcgcatgtac gactcatat ctgacgcgca gcctctgctg ctcagcacct tcagcggaga
2221 ccgccgcttc tccgatttg gtggcgttct gcaattgagt gacctggatg atgatggctt
2281 agatgaaatc atcatggcag cccccctgag gatagcagat gtaacctctg gactgattgg
2341 gggagaagac ggccgagtat atgtatataa tggcaaaagag accacccttg gtgacatgac
2401 tggcaaatgc aaatcatgga taactccatg tccagaagaa aaggtaatg aaaaaaaaaa
2461 aaaaaaaaaa aa

FIG. 5B

FIG. 6A
FIG. 6B

FIG. 6A

SEQ ID NO: 15

1942 bp: 455 a 496 c 502 g 489 t

FIG. 6

1 gggctgtaac tctgccatcc ctacagcataa ttggggggta tgatttcact atcctaattg
61 cctgtccctaa gtgattccttac ttgctgatatg gacctaatgt tttattttat tgttttagcac
121 ttctaaaaaac tcattttcctt tacacaaagtc caatactttg gacaggaaac agtagctttg
181 ttgattatgc tacgtgtctt tactgtctat aatgattcctt ttatttcagg attccatgtc
241 ctttatctac aaggctttgg aaaggaacat aaggacaatg ttcatagggtg gctctcagtt
301 gtcacaaaag cacgtctcca gcccttagc atcttacttc ttgtcatttc cttatgcgag
361 gcttggctgg gcaatgacct cagctgacct caaccaggat gggcacggtg acctcgtggt
421 gggcgcacca ggctacagcc gccccggcca catccacatc gggcgctgt acctcatcta
481 cggcaatgac ctgggcctgc cacctgttga cctggacctg gacaaggagg cccacaggat
541 ccttgaaggc ttccagccct caggtcggtt tggctcggcc ttggctgtgt tggacttttaa
601 cgtggacggc gtgcctgacc tggccgtggg agctccctcg gtgggctccg agcagctcac
661 ctacaaaagg gccgtgtatg tctactttgg ttccaaacaa ggagggaatgt ctcttcccc
721 taacatcacc atttcttgcc aggacatcta ctgtaacttg ggctggactc tcttggctgc

781 agatgtgaat ggagacagtg aaccgatct ggtcatcggc tccccttttg caccaggtgg
841 agggaaagcag aagggaattg tggctgcgtt ttattctggc ccagcctga gcgacaaaga
901 aaaactgaac gtggaggcag ccaactggac ggtgagaggc gaggaagact tctcctggtt
961 tggatatcc ctacaggtg tcaactgtga caacagaacc ttgctgttgg ttgggagccc
1021 gacctggaag aatgccagca ggctgggcca tttgttacac atccgagatg agaaaaagag
1081 ccttgggagg gtgtatggct acttcccacc aaacggccaa agctggttta ccatttctgg
1141 agacaaaggca atgggaaac tgggtacttc cctttccagt ggccacgtac tgatgaatgg
1201 gactctgaaa caagtgtgc tggttggagc cctacgtac gatgacgtgt ctaagggtggc
1261 attcctgacc gtgacctac accaaggcgg agccactcgc atgtacgcac tcatatctga
1321 cgcgcagcct ctgctgctca gcaccttcag cggagaccgc cgcttctccc gatttgggtgg
1381 cgttctgcac ttgagtgacc tggatgatga tggcttagat gaaatcatca tggcagcccc
1441 cctgaggata gcagatgtaa cctctggact gattgggga gaagacggcc gagtatatgt
1501 atataatggc aaagagacca cccttgggtga catgactggc aaatgcaaat catggataac
1561 tccatgtcca gaagaaaagg cccaatatgt attgatttct cctgaagcca gctcaagggtt
1621 tgggagctcc ctcatcaccg tgagggtccaa ggcaaaagaa caagtctgta ttgctgctgg
1681 aaggagtctt ttgggagccc gactctccgg ggcacttcac gtctatagcc ttggctcaga
1741 ttgaagattt cactgcattt cccactctg cccacctctc tcatgctgaa tcacatccat
1801 ggtgagcatt ttgatggaca aagtggcaca tccagtggag cggtaggtaga tcctgataga
1861 catggggctc ctgggagtag agagacacac taacagccac accctctgga aatctgatac
1921 agtaaatata tgactgcacc ag

FIG. 6B

SEQ ID NO: 16 database	MSAFRLWPGLLIMLGSLCHRGSPCGLSTHVEIGHRALEFLQLHNGRVNYRELLEHQDAY	60
SEQ ID NO: 17 d3	-----	-----
SEQ ID NO: 18 b2	MSAFRLWPGLLIMLGSLCHRGSPCGLSTHVEIGHRALEFLQLHNGRVNYRELLEHQDAY	60
SEQ ID NO: 19 a1	MSAFRLWPGLLIMLGSLCHRGSPCGLSTHVEIGHRALEFLQLHNGRVNYRELLEHQDAY	60
database	QAGIVFPDCFYPSICKGKGFHDVSESTHWTFFLNASVHYIRENYPLPWEKDTKLVAFLF	120
d3	-----	-----
b2	QAGIVFPDCFYPSICKGKGFHDVSESTHWTFFLNASVHYIRENYPLPWEKDTKLVAFLF	120
a1	QAGIVFPDCFYPSICKGKGFHDVSESTHWTFFLNASVHYIRENYPLPWEKDTKLVAFLF	120
database	GITSHMAADVSWHSLGLEQGFRLRTMGAIDFHGSYSEAHSAAGDFGGDVLSQFEFNFNYLAR	180
d3	-----	-----
b2	GITSHMAADVSWHSLGLEQGFRLRTMGAIDFHGSYSEAHSAAGDFGGDVLSQFEFNFNYLAR	180
a1	GITSHMAADVSWHSLGLEQGFRLRTMGAIDFHGSYSEAHSAAGDFGGDVLSQFEFNFNYLAR	180
database	RWYVPVKDLLGIYEKLYGRKVIITENVIVDCSHIQFLEMYGEMLAVSKLYPTYSTKSPFLV	240
d3	-----	-----
b2	RWYVPVKDLLGIYEKLYGRKVIITENVIVDCSHIQFLEMYGEMLAVSKLYPTYSTKSPFLV	240
a1	RWYVPVKDLLGIYEKLYGRKVIITENVIVDCSHIQFLEMYGEMLAVSKLYPTYSTKSPFLV	240
database	EQFQEYFLGGLDDMAFWSTNIYHLTSMLENGTSDCNLPENPLFIACGGQQNHTQGSKMQ	300
d3	-----	-----
b2	EQFQEYFLGGLDDMAFWSTNIYHLTSMLENGTSDCNLPENPLFIACGGQQNHTQGSKMQ	300
a1	EQFQEYFLGGLDDMAFWSTNIYHLTSMLENGTSDCNLPENPLFIACGGQQNHTQGSKMQ	300

FIG. 7A
FIG. 7B
FIG. 7C

FIG. 7A

FIG. 7

database	KNDFHRNLTTSLTESVDRNININITERGVFFSVNSWTPDMSFSIYKALERNIRTMFIGGSQ	360
d3	-----MILLFQDSMSFSIYKALERNIRTMFIGGSQ	30
b2	KNDFHRNLTTSLTESVDRNININITERGVFFSVNSWTPDMSFSIYKALERNIRTMFIGGSQ	360
a1	KNDFHRNLTTSLTESVDRNININITERGVFFSVNSWTPDMSFSIYKALERNIRTMFIGGSQ	360
database	SQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIY	420
d3	SQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIY	90
b2	SQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIY	420
a1	SQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIY	420
database	GNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDFNVDPDLAVGAPSVGSEQLT	480
d3	GNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDFNVDPDLAVGAPSVGSEQLT	150
b2	GNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDFNVDPDLAVGAPSVGSEQLT	480
a1	GNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDFNVDPDLAVGAPSVGSEQLT	480
database	YKGAVVYVYFGSKQGMSSSPNITISCQDIYCNLGTLLAADVNGDSEPDLVIGSPFAPGG	540
d3	YKGAVVYVYFGSKQGMSSSPNITISCQDIYCNLGTLLAADVNGDSEPDLVIGSPFAPGG	210
b2	YKGAVVYVYFGSKQGMSSSPNITISCQDIYCNLGTLLAADVNGDSEPDLVIGSPFAPGG	540
a1	YKGAVVYVYFGSKQGMSSSPNITISCQDIYCNLGTLLAADVNGDSEPDLVIGSPFAPGG	540
database	GKQKGIVAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTLLLVGSP	600
d3	GKQKGIVAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTLLLVGSP	270
b2	GKQKGIVAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTLLLVGSP	600
a1	GKQKGIVAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTLLLVGSP	600

FIG. 7B

database	TWKNASRLGHLHLHIRDEKKS LGRVGYGFPNQGQSWFTISGDKAMGKLGTSLSSGHVLMNG	660
d3	TWKNASRLGHLHLHIRDEKKS LGRVGYGFPNQGQSWFTISGDKAMGKLGTSLSSGHVLMNG	330
b2	TWKNASRLGHLHLHIRDEKKS LGRVGYGFPNQGQSWFTISGDKAMGKLGTSLSSGHVLMNG	660
a1	TWKNASRLGHLHLHIRDEKKS LGRVGYGFPNQGQSWFTISGDKAMGKLGTSLSSGHVLMNG	660
database	TLKQVLLVGAPTYDDVSKVAF LTVTLHQGGATRM YALISDAQPLLLSTFSGDRRFSRFGG	720
d3	TLKQVLLVGAPTYDDVSKVAF LTVTLHQGGATRM YALISDAQPLLLSTFSGDRRFSRFGG	390
b2	TLKQVLLVGAPTYDDVSKVAF LTVTLHQGGATRM YALISDAQPLLLSTFSGDRRFSRFGG	720
a1	TLKQVLLVGAPTYDDVSKVAF LTVTLHQGGATRM YALISDAQPLLLSTFSGDRRFSRFGG	720
database	VLHLSDLDDGLDEI IMAAPLRIADVTSLIGGEDGRV VYVYNGKETTLGDMTGKCKSWIT	780
d3	VLHLSDLDDGLDEI IMAAPLRIADVTSLIGGEDGRV VYVYNGKETTLGDMTGKCKSWIT	450
b2	VLHLSDLDDGLDEI IMAAPLRIADVTSLIGGEDGRV VYVYNGKETTLGDMTGKCKSWIT	780
a1	VLHLSDLDDGLDEI IMAAPLRIADVTSLIGGEDGRV VYVYNGKETTLGDMTGKCKSWIT	780
database	PCPEEKAQYVVLISPEASSRFGSSLITVRSKAKNQV VIAAGRSSLGALH VYSLGSD	840
d3	PCPEEKAQYVVLISPEASSRFGSSLITVRSKAKNQV VIAAGRSSLGALH VYSLGSD	510
b2	PCPEEKVSEKKKKK-----	795
a1	PCPEEKAQYVVLISPEASSRFGSSLITVRSKAKNQV VIAAGRSSLGALH VYSLGSD	840
Database	840 aa	
d3	510 aa	
b2	795 aa	
a1	840 aa	

FIG. 7C

FIG. 8A
FIG. 8B
FIG. 8C
FIG. 8D
FIG. 8E
FIG. 8F
FIG. 8G
FIG. 8H
FIG. 8I
FIG. 8J
FIG. 8K
FIG. 8L

FIG. 8

1: pancreatic-form: cDNA sequence from GenBank database (L11702) SEQ ID NO: 20
2: cDNA clone A1 SEQ ID NO: 21
3: cDNA clone B2 SEQ ID NO: 22
4: cDNA clone D3 SEQ ID NO: 23

1 GTGACCTGCTTAGAGAGAGCGGTGGTCTGCACCTGGATTTTGGAGTCCCAGTGTGCT 60
1 -----GTCAGCACCTGGATTTTGGAGTCCCAGTGTGCT 34

1 -----ATGCTGTGCT 9
61 GCAGCTCTGAGCATCCACGTCACAGAGAAGCCGGTGGCAATGAGAGCATGTCTGCT 120
35 GCAGCTCTGAGCATCCACGTCACAGAGAAGCCGGTGGCAATGAGAGCATGTCTGCT 94

10 TTCAGGTTGTGGCCTGGCCTGCTGATCATGTTGGGTTCTCTGCCATAGAGGTTACCCG 69
121 TTCAGGTTGTGGCCTGGCCTGCTGATCATGTTGGGTTCTCTGCCATAGAGGTTACCCG 180
95 TTCAGGTTGTGGCCTGGCCTGCTGATCATGTTGGGTTCTCTGCCATAGAGGTTACCCG 154

70 TGTGGCCTTTCAACACACAGTAGAATAAGGACACAGAGCTCTGGAGTTTCTTCAGCTTCAC 129
181 TGTGGCCTTTCAACACACACATAGAATAAGGACACAGAGCTCTGGAGTTTCTTCAGCTTCAC 240
155 TGTGGCCTTTCAACACACATAGAATAAGGACACAGAGCTCTGGAGTTTCTTCAGCTTCAC 214

FIG. 8A

130 AATGGCGGTGTTAACTACAGAGAGCTGTTACTAGAAACACCAGGATGCGTATCAGGCTGGA 189
241 AATGGCGGTGTTAACTACAGAGAGCTGTTACTAGAAACACCAGGATGCGTATCAGGCTGGA 300
215 AATGGCGGTGTTAACTACAGAGAGCTGTTACTAGAAACACCAGGATGCGTATCAGGCTGGA 274

190 ATCGTGTTTCCTGATTGTTTTTACCCTAGCATCTGCAAAGGAGGAAAAATTCATGATGTG 249
301 ATCGTGTTTCCTGATTGTTTTTACCCTAGCATCTGCAAAGGAGGAAAAATTCATGATGTG 360
275 ATCGTGTTTCCTGATTGTTTTTACCCTAGCATCTGCAAAGGAGGAAAAATTCATGATGTG 334

250 TCTGAGAGCACTCACTGGACTCCGTTTCTTAATGCAAGCGTTCATTATATCCGAGAGAAC 309
361 TCTGAGAGCACTCACTGGACTCCGTTTCTTAATGCAAGCGTTCATTATATCCGAGAGAAC 420
335 TCTGAGAGCACTCACTGGACTCCGTTTCTTAATGCAAGCGTTCATTATATCCGAGAGAAC 394

310 TATCCCCCTTCCCTGGGAGAGGACACAGAGAAACTGGTAGCTTCTTGTGGAATTACT 369
421 TATCCCCCTTCCCTGGGAGAGGACACAGAGAAACTGGTAGCTTCTTGTGGAATTACT 480
395 TATCCCCCTTCCCTGGGAGAGGACACAGAGAAACTGGTAGCTTCTTGTGGAATTACT 454

370 TCTCACATGGCGGCAGATGTCAGCTGGCATACTGTGGGCCCTTGAAACAAGGATTCCTTAGG 429
481 TCTCACATGGCGGCAGATGTCAGCTGGCATACTGTGGGCCCTTGAAACAAGGATTCCTTAGG 540
541 TCTCACATGGCGGCAGATGTCAGCTGGCATACTGTGGGCCCTTGAAACAAGGATTCCTTAGG 514

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FIG. 8B

430 ACCATGGGAGCTATTGATTTTTCACGGCTCCTATTTCAGAGGCTCATTCGGCTGGTGATTTT 489
541 ACCATGGGAGCTATTGATTTTTCACGGCTCCTATTTCAGAGGCTCATTCGGCTGGTGATTTT 600
515 ACCATGGGAGCTATTGATTTTTCACGGCTCCTATTTCAGAGGCTCATTCGGCTGGTGATTTT 574

490 GGAGGAGATGTGTTGAGCCAGTTTGAAATTTTAATTTTAAATTACCTTGACGACGCTGGTAT 549
601 GGAGGAGATGTGTTGAGCCAGTTTGAAATTTTAATTTTAAATTACCTTGACGACGCTGGTAT 660
575 GGAGGAGATGTGTTGAGCCAGTTTGAAATTTTAATTTTAAATTACCTTGACGACGCTGGTAT 634

550 GTGCCAGTCAAAGATCTACTGGGAAATTTATGAGAAACTGTATGGTCGAAAGTCATCACC 609
661 GTGCCAGTCAAAGATCTACTGGGAAATTTATGAGAAACTGTATGGTCGAAAGTCATCACC 720
635 GTGCCAGTCAAAGATCTACTGGGAAATTTATGAGAAACTGTATGGTCGAAAGTCATCACC 694

610 GAAAATGTAATCGTTGATTGTTACATATCCAGTTCTTAGAAATGTATGGTGAGATGCTA 669
721 GAAAATGTAATCGTTGATTGTTACATATCCAGTTCTTAGAAATGTATGGTGAGATGCTA 780
695 GAAAATGTAATCGTTGATTGTTACATATCCAGTTCTTAGAAATGTATGGTGAGATGCTA 754

670 GCTGTTTCCAAGTTATATATCCCACTTACTCTACAAAGTCCCCGTTTTTTGGTGGAACAATTC 729
781 GCTGTTTCCAAGTTATATATCCCACTTACTCTACAAAGTCCCCGTTTTTTGGTGGAACAATTC 840
755 GCTGTTTCCAAGTTATATATCCCACTTACTCTACAAAGTCCCCGTTTTTTGGTGGAACAATTC 814

FIG. 8C

730 CAAGAGTATTTTCTTGGAGGACTGGATGATATGGCATTTTGGTCCACTAATAATTTACCAT 789
841 CAAGAGTATTTTCTTGGAGGACTGGATGATATGGCATTTTGGTCCACTAATAATTTACCAT 900
815 CAAGAGTATTTTCTTGGAGGACTGGATGATATGGCATTTTGGTCCACTAATAATTTACCAT 874
-----GGGCTGTAAC 10
790 CTAAACAATCTTCATGTTGGAGAAATGGGACCAGTGACTGCAACCTGCCCTGAGAACCCCTCTG 849
901 CTAAACAAGCTTTCATGTTGGAGAAATGGGACCAGTGACTGCAACCTGCCCTGAGAACCCCTCTG 960
875 CTAAACAAGCTTTCATGTTGGAGAAATGGGACCAGTGACTGCAACCTGCCCTGAGAACCCCTCTG 934
11 TCTGCCATCCCTCAGCATAAATTTGGGGGTATGATTTTCACTATCCTAATTGCCCTGTCCCTAA 70
850 TTCAATTGCATGTGGCGGCCAGCAAAACCAACCCAGGGCTCAAAAATGCAGAAAAATGAT 909
961 TTCAATTGCATGTGGCGGCCAGCAAAACCAACCCAGGGCTCAAAAATGCAGAAAAATGAT 1020
935 TTCAATTGCATGTGGCGGCCAGCAAAACCAACCCAGGGCTCAAAAATGCAGAAAAATGAT 994
71 GTGATCCTTACTTGCTGATAGGACCCTAAATGTTTATTTATTTAGCACTTCTCTAAAAAAC 130
910 TTTTCACAGAAATTTGACTACATCCCTAACTGAAAGTGTGACAGGAAATATAAACTATACT 969
1021 TTTTCACAGAAATTTGACTACATCCCTAACTGAAAGTGTGACAGGAAATATAAACTATACT 1080
995 TTTTCACAGAAATTTGACTACATCCCTAACTGAAAGTGTGACAGGAAATATAAACTATACT 1054
131 TCATTTCCCTTTACACAAGTCCAATACTTTGGACAGGAAACAGTAGCTTTGTTGATTATGC 180
970 GAAAGAGGAGTGTTCTTTAGTGTAATAATTCCTGGACCCCGGATTCCCATGTCCCTTTATCTAC 1029
1081 GAAAGAGGAGTGTTCTTTAGTGTAATAATTCCTGGACCCCGGATTCCCATGTCCCTTTATCTAC 1140
1055 GAAAGAGGAGTGTTCTTTAGTGTAATAATTCCTGGACCCCGGATTCCCATGTCCCTTTATCTAC 1114
181 TACGTGCTTTACTGCTATAATGATTCCTTTTATTTTCAGGATTCCCATGTCCCTTTATCTAC 240

FIG. 8D

1030 AAGGCTTTGGAAGGAACATAAGGACAAATGTTCATAGGTGGCTCTCAGTTGTCACAAAG 1089
1141 AAGGCTTTGGAAGGAACATAAGGACAAATGTTCATAGGTGGCTCTCAGTTGTCACAAAG 1200
1115 AAGGCTTTGGAAGGAACATAAGGACAAATGTTCATAGGTGGCTCTCAGTTGTCACAAAG 1174
241 AAGGCTTTGGAAGGAACATAAGGACAAATGTTCATAGGTGGCTCTCAGTTGTCACAAAG 300

1090 CACGTCTCCAGCCCCCTTAGCATCTTACTTCTTGTCATTTCCCTTATGCGAGGCTTGGCTGG 1149
1201 CACGTCTCCAGCCCCCTTAGCATCTTACTTCTTGTCATTTCCCTTATGCGAGGCTTGGCTGG 1260
1175 CACGTCTCCAGCCCCCTTAGCATCTTACTTCTTGTCATTTCCCTTATGCGAGGCTTGGCTGG 1234
301 CACGTCTCCAGCCCCCTTAGCATCTTACTTCTTGTCATTTCCCTTATGCGAGGCTTGGCTGG 360

1150 GCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGGTGGCGCACCA 1209
1261 GCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGGTGGCGCACCA 1320
1235 GCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGGTGGCGCACCA 1294
361 GCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGGTGGCGCACCA 420

1210 GGCTACAGCCGCCCGGCCACATCCACATCGGGCGCGTGACCTCATCTACGGCAATGAC 1269
1321 GGCTACAGCCGCCCGGCCACATCCACATCGGGCGCGTGACCTCATCTACGGCAATGAC 1380
1295 GGCTACAGCCGCCCGGCCACATCCACATCGGGCGCGTGACCTCATCTACGGCAATGAC 1354
421 GGCTACAGCCGCCCGGCCACATCCACATCGGGCGCGTGACCTCATCTACGGCAATGAC 480

1270 CTGGGCCCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCCAACAGGATCCTTGAAGGC 1329
1381 CTGGGCCCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCCAACAGGATCCTTGAAGGC 1440
1355 CTGGGCCCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCCAACAGGATCCTTGAAGGC 1414
481 CTGGGCCCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCCAACAGGATCCTTGAAGGC 540

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FIG. 8E

1330 TTCCAGCCCTCAGGTCGGTTTGGCTCGGCCCTTGGCTGTGTTGGACTTTAAACGTGGACGGC 1389
1441 TTCCAGCCCTCAGGTCGGTTTGGCTCGGCCCTTGGCTGTGTTGGACTTTAAACGTGGACGGC 1500
1415 TTCCAGCCCTCAGGTCGGTTTGGCTCGGCCCTTGGCTGTGTTGGACTTTAAACGTGGACGGC 1474
541 TTCCAGCCCTCAGGTCGGTTTGGCTCGGCCCTTGGCTGTGTTGGACTTTAAACGTGGACGGC 600

1390 GTGCCTGACCTGGCCGTGGAGCTCCCTCGGTGGGCTCCGAGCAGCTCACCTACAAAGGT 1449
1501 GTGCCTGACCTGGCCGTGGAGCTCCCTCGGTGGGCTCCGAGCAGCTCACCTACAAAGGT 1560
1475 GTGCCTGACCTGGCCGTGGAGCTCCCTCGGTGGGCTCCGAGCAGCTCACCTACAAAGGT 1534
601 GTGCCTGACCTGGCCGTGGAGCTCCCTCGGTGGGCTCCGAGCAGCTCACCTACAAAGGT 660

1450 GCCGTGATGTCTACTTTGGTTCCAAACAAGAGGAATGTCTTCTTCCCCCTAACATCACC 1509
1561 GCCGTGATGTCTACTTTGGTTCCAAACAAGAGGAATGTCTTCTTCCCCCTAACATCACC 1620
1535 GCCGTGATGTCTACTTTGGTTCCAAACAAGAGGAATGTCTTCTTCCCCCTAACATCACC 1594
661 GCCGTGATGTCTACTTTGGTTCCAAACAAGAGGAATGTCTTCTTCCCCCTAACATCACC 720

1510 ATTTCTTGCCAGGACATCTACTGTAACTTGGCTGGACTCTCTTGGCTGCAGATGTGAAT 1569
1621 ATTTCTTGCCAGGACATCTACTGTAACTTGGCTGGACTCTCTTGGCTGCAGATGTGAAT 1680
1595 ATTTCTTGCCAGGACATCTACTGTAACTTGGCTGGACTCTCTTGGCTGCAGATGTGAAT 1654
721 ATTTCTTGCCAGGACATCTACTGTAACTTGGCTGGACTCTCTTGGCTGCAGATGTGAAT 780

1570 GGAGACAGTGAAACCCGATCTGGTCATCGGCTCCCCCTTTTGCAACCAGGTGGAGGGAAGCAG 1629
1681 GGAGACAGTGAAACCCGATCTGGTCATCGGCTCCCCCTTTTGCAACCAGGTGGAGGGAAGCAG 1740
1655 GGAGACAGTGAAACCCGATCTGGTCATCGGCTCCCCCTTTTGCAACCAGGTGGAGGGAAGCAG 1714
781 GGAGACAGTGAAACCCGATCTGGTCATCGGCTCCCCCTTTTGCAACCAGGTGGAGGGAAGCAG 840

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FIG. 8F

1630 AAGGGAATTGTGGCTGCGTTTATTCTGGCCCCAGCCTGAGCGACAAAGAAAACTGAAC 1689
1741 AAGGGAATTGTGGCTGCGTTTATTCTGGCCCCAGCCTGAGCGACAAAGAAAACTGAAC 1800
1715 AAGGGAATTGTGGCTGCGTTTATTCTGGCCCCAGCCTGAGCGACAAAGAAAACTGAAC 1774
841 AAGGGAATTGTGGCTGCGTTTATTCTGGCCCCAGCCTGAGCGACAAAGAAAACTGAAC 900
1690 GTGGAGGCAGCCAACTGGACGGTGAGAGCGGAGGAAGACTTCTCCTGGTTTGGATATTCC 1749
1801 GTGGAGGCAGCCAACTGGACGGTGAGAGCGGAGGAAGACTTCTCCTGGTTTGGATATTCC 1860
1775 GTGGAGGCAGCCAACTGGACGGTGAGAGCGGAGGAAGACTTCTCCTGGTTTGGATATTCC 1834
901 GTGGAGGCAGCCAACTGGACGGTGAGAGCGGAGGAAGACTTCTCCTGGTTTGGATATTCC 960
1750 CTTACGGGTGCTACTGTGGACAACAGAAACCTTGCTGTTGTTGGAGCCCCGACCTGGAAG 1809
1861 CTTACGGGTGCTACTGTGGACAACAGAAACCTTGCTGTTGTTGGAGCCCCGACCTGGAAG 1920
1835 CTTACGGGTGCTACTGTGGACAACAGAAACCTTGCTGTTGTTGGAGCCCCGACCTGGAAG 1894
961 CTTACGGGTGCTACTGTGGACAACAGAAACCTTGCTGTTGTTGGAGCCCCGACCTGGAAG 1020
1810 AATGCCAGCAGGCTGGGCCATTGTGTACACATCCGAGATGAGAAAGAGCCTTGGGAGG 1869
1921 AATGCCAGCAGGCTGGGCCATTGTGTACACATCCGAGATGAGAAAGAGCCTTGGGAGG 1980
1895 AATGCCAGCAGGCTGGGCCATTGTGTACACATCCGAGATGAGAAAGAGCCTTGGGAGG 1954
1021 AATGCCAGCAGGCTGGGCCATTGTGTACACATCCGAGATGAGAAAGAGCCTTGGGAGG 1080
1870 GTGTATGGCTACTTCCCAACCAACGGCCAAAGCTGGTTTACCATTTCTGGAGACAAGGCA 1929
1981 GTGTATGGCTACTTCCCAACCAACGGCCAAAGCTGGTTTACCATTTCTGGAGACAAGGCA 2040
1955 GTGTATGGCTACTTCCCAACCAACGGCCAAAGCTGGTTTACCATTTCTGGAGACAAGGCA 2014
1081 GTGTATGGCTACTTCCCAACCAACGGCCAAAGCTGGTTTACCATTTCTGGAGACAAGGCA 1140

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FIG. 8G

1930 ATGGGGAAACTGGGTACTTCCCTTCCAGTGGCCACGTACTGATGAATGGGACTCTGAAA 1989
2041 ATGGGGAAACTGGGTACTTCCCTTCCAGTGGCCACGTACTGATGAATGGGACTCTGAAA 2100
2015 ATGGGGAAACTGGGTACTTCCCTTCCAGTGGCCACGTACTGATGAATGGGACTCTGAAA 2074
1141 ATGGGGAAACTGGGTACTTCCCTTCCAGTGGCCACGTACTGATGAATGGGACTCTGAAA 1200
1990 CAAGTGCTGCTGGTTGGAGCCCCCTACGTACGATGACGTGTCTAAGGTGGCATTCCTGACC 2049
2101 CAAGTGCTGCTGGTTGGAGCCCCCTACGTACGATGACGTGTCTAAGGTGGCATTCCTGACC 2160
2075 CAAGTGCTGCTGGTTGGAGCCCCCTACGTACGATGACGTGTCTAAGGTGGCATTCCTGACC 2134
1201 CAAGTGCTGCTGGTTGGAGCCCCCTACGTACGATGACGTGTCTAAGGTGGCATTCCTGACC 1260
2050 GTGACCCCTACACCAAGGGGGAGCCACTCGCATGTACGCACCTCATATCTGACGCGCAGCCT 2109
2161 GTGACCCCTACACCAAGGGGGAGCCACTCGCATGTACGCACCTCATATCTGACGCGCAGCCT 2220
2135 GTGACCCCTACACCAAGGGGGAGCCACTCGCATGTACGCACCTCATATCTGACGCGCAGCCT 2194
1261 GTGACCCCTACACCAAGGGGGAGCCACTCGCATGTACGCACCTCATATCTGACGCGCAGCCT 1320
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2110 CTGCTGCTCAGCACCTTCAGCGGAGACCGCCGCTTCTCCCGATTGTTGGTGGCGTTCTGCAC 2169
2221 CTGCTGCTCAGCACCTTCAGCGGAGACCGCCGCTTCTCCCGATTGTTGGTGGCGTTCTGCAC 2280
2195 CTGCTGCTCAGCACCTTCAGCGGAGACCGCCGCTTCTCCCGATTGTTGGTGGCGTTCTGCAC 2254
1321 CTGCTGCTCAGCACCTTCAGCGGAGACCGCCGCTTCTCCCGATTGTTGGTGGCGTTCTGCAC 1380
2170 TTGAGTGACCTGGATGATGATGGCTTAGATGAAATCATCATGGCAGCCCCCTGAGGATA 2229
2281 TTGAGTGACCTGGATGATGATGGCTTAGATGAAATCATCATGGCAGCCCCCTGAGGATA 2340
2255 TTGAGTGACCTGGATGATGATGGCTTAGATGAAATCATCATGGCAGCCCCCTGAGGATA 2314
1381 TTGAGTGACCTGGATGATGATGGCTTAGATGAAATCATCATGGCAGCCCCCTGAGGATA 1440

FIG. 8H

2230	GCAGATGTAACCTCTGGACTGTATTGGGGAGAAGACGCCCGAGTATATGTATAATAATGGC	2289
2341	GCAGATGTAACCTCTGGACTGTATTGGGGAGAAGACGCCCGAGTATATGTATAATAATGGC	2400
2315	GCAGATGTAACCTCTGGACTGTATTGGGGAGAAGACGCCCGAGTATATGTATAATAATGGC	2374
1441	GCAGATGTAACCTCTGGACTGTATTGGGGAGAAGACGCCCGAGTATATGTATAATAATGGC	1500
2290	AAAGAGACCACCCCTTGTTGACATGACTGGCAAATGCAAAATCATGGATAA C TCCATGTCCA	2349
2401	AAAGAGACCACCCCTTGTTGACATGACTGGCAAATGCAAAATCATGGATAA C TCCATGTCCA	2460
2375	AAAGAGACCACCCCTTGTTGACATGACTGGCAAATGCAAAATCATGGATAA C TCCATGTCCA	2434
1501	AAAGAGACCACCCCTTGTTGACATGACTGGCAAATGCAAAATCATGGATAA C TCCATGTCCA	1560
2350	GAAGAAAAGGCCCAATATGTATTGATTTCTCTGAAGCCAGCTCAAGGTTTGGGAGCTCC	2409
2461	GAAGAAAAGGCCCAATATGTATTGATTTCTCTGAAGCCAGCTCAAGGTTTGGGAGCTCC	2520
2435	GAAGAAAAGGTAAGTGAAAAA AAAAAAAAA-----	2472
1561	GAAGAAAAGGCCCAATATGTATTGATTTCTCTGAAGCCAGCTCAAGGTTTGGGAGCTCC	1620
2410	CTCATCACCGTGAGGTCCAAGGCCAAAGAACCAAGTCGTCATTGCTGCTGGAAGGAGTTCT	2469
2521	CTCATCACCGTGAGGTCCAAGGCCAAAGAACCAAGTCGTCATTGCTGCTGGAAGGAGTTCT	2580

1621	CTCATCACCGTGAGGTCCAAGGCCAAAGAACCAAGTCGTCATTGCTGCTGGAAGGAGTTCT	1680
2470	TTGGGAGCCCCGACTCTCCGGGGCACTTCACGCTCTATAGCCCTTGGCTCAGATTGAAGATTT	2529
2581	TTGGGAGCCCCGACTCTCCGGGGCACTTCACGCTCTATAGCCCTTGGCTCAGATTGAAGATTT	2640

1681	TTGGGAGCCCCGACTCTCCGGGGCACTTCACGCTCTATAGCCCTTGGCTCAGATTGAAGATTT	1740

F.G. 8

2530	CACTGCATTTCCCACTCTGCCCACCTCTCTCATGCTGAATCACATCCATGGTGAGCATT	2589
2641	CACTGCATTTCCCACTCTGCCCACCTCTCTCATGCTGAATCACATCCATGGTGAGCATT	2700

1741	CACTGCATTTCCCACTCTGCCCACCTCTCTCATGCTGAATCACATCCATGGTGAGCATT	1800
2590	TTGATGGACAAAGTGGCACATCCAGTGGGCTGTAGATCCTGATAGACATGGGGCTC	2649
2701	TTGATGGACAAAGTGGCACATCCAGTGGGCTGTAGATCCTGATAGACATGGGGCTC	2760

1801	TTGATGGACAAAGTGGCACATCCAGTGGGCTGTAGATCCTGATAGACATGGGGCTC	1860
2650	CTGGGAGTAGAGAGACACACTAACAGCCACACCCCTCTGGAAATCTGATACAGTAAATATA	2709
2761	CTGGGAGTAGAGAGACACACTAACAGCCACACCCCTCTGGAAATCTGATACAGTAAATATA	2820

1861	CTGGGAGTAGAGAGACACACTAACAGCCACACCCCTCTGGAAATCTGATACAGTAAATATA	1920
2710	TGACTGCACCCAGAAAATATGTGAAAATAGCAGACATTCTGCTTACTCATGTCTCCTTCCACA	2769
2821	TGACTGCACCCAGAAAATATGTGAAAATAGCAGACATTCTGCTTACTCATGTCTCCTTCCACA	2880

1921	TGACTGCACCCAGAAAATATGTGAAAATAGCAGACATTCTGCTTACTCATGTCTCCTTCCACA	1952

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FIG. 8J

2770 GTTACTTCCTCGCTCCCTTTGCACTAAACCTTTCTTCTTTCCCAACTTATTGCCTGTA 2829
2881 AAAAAAAAAAAAAAAAAAAAAA----- 2915

2830 GTCAGACCTGCTGTACAACCTATTTCCTCTCTTGAATGTCTTCCAGTGGCTGGAA 2889

2890 AGTCCCCTCTGTGTTATCTGTAGAACAGTCTCTGTACACAATTCCCTCTAAACATC 2949

2950 CTTTTTAAAAAGAAATTGTTTCAGCCATAAAGAAAGAACAGATCATGCCCTTTCAGAG 3009

3010 GACATGGATGGAGCTGGAGGCCATTATCCTTCATAAACTATTGCAGGAACAGAAACCAA 3069

FIG. 8K

3070 AACTCCATATTCTCACTTGTAAGTGGAGCTAAGTGAGAACACGTGGACACATAGAGGG 3129

3130 AAACAACACACTGGGGCCTATGAGAGGCGGAAGGTGGAGGAGAGATCAGGAA 3189

3190 AAATAACTAATGGATACTTAGGGTGATGAAATAATCTGTGTAACAAACCCCATGACACA 3249

3250 CCTTTATGTATGTAACAAACCAGCACTTCCTGCGCATGTACCCCTGAACTTAAAGTTAA 3309

3310 AAAAAGTTGAACCTTAAAAATAACAGATTGGCCCATGCCCAATCAAAGTATAATAGAAAGC 3369

3370 ATAGTATAC 3378

FIG. 8L